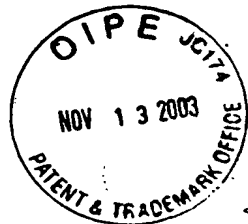


#8



1

SEQUENCE LISTING

<110> BRASLAWSKY, GARY R.
HANNA, NABIL
CHINN, PAUL

<120> ENGINEERED TETRAVALENT ANTIBODIES AND METHODS OF USE

<130> 037003-0280727

<140> 10/058,069

<141> 2002-01-29

<150> 60/341,858

<151> 2001-12-21

<150> 60/264,318

<151> 2001-01-29

<150> 60/331,481

<151> 2001-11-16

<160> 17

<170> PatentIn Ver. 2.1

<210> 1

<211> 470

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic C2B8
heavy chain amino acid sequence

<400> 1

Met	Gly	Trp	Ser	Leu	Ile	Leu	Leu	Phe	Leu	Val	Ala	Val	Ala	Thr	Arg
1				5					10					15	
Val	Leu	Ser	Gln	Val	Gln	Leu	Gln	Gln	Pro	Gly	Ala	Glu	Leu	Val	Lys
			20					25					30		
Pro	Gly	Ala	Ser	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe
		35					40					45			
Thr	Ser	Tyr	Asn	Met	His	Trp	Val	Lys	Gln	Thr	Pro	Gly	Arg	Gly	Leu
		50				55					60				
Glu	Trp	Ile	Gly	Ala	Ile	Tyr	Pro	Gly	Asn	Gly	Asp	Thr	Ser	Tyr	Asn
	65				70				75						80
Gln	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Ala	Asp	Lys	Ser	Ser	Ser
			85						90					95	
Thr	Ala	Tyr	Met	Gln	Leu	Ser	Ser	Leu	Thr	Ser	Glu	Asp	Ser	Ala	Val
			100					105						110	

Tyr	Tyr	Cys	Ala	Arg	Ser	Thr	Tyr	Tyr	Gly	Gly	Asp	Trp	Tyr	Phe	Asn
		115					120					125			
Val	Trp	Gly	Ala	Gly	Thr	Thr	Val	Thr	Val	Ser	Ala	Ala	Ser	Thr	Lys
	130					135					140				
Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly
145					150					155					160
Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro
				165					170					175	
Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr
			180					185					190		
Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val
		195					200					205			
Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn
	210					215					220				
Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Ala	Glu	Pro
225					230					235					240
Lys	Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu
				245					250					255	
Leu	Leu	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp
			260					265					270		
Thr	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp
		275					280					285			
Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly
	290					295					300				
Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn
305					310					315					320
Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp
				325					330					335	
Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro
			340					345					350		
Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu
		355					360					365			
Pro	Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn
	370					375					380				
Gln	Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile
385					390					395					400
Ala	Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr
				405					410					415	

Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
 420 425 430

Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
 435 440 445

Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
 450 455 460

Ser Leu Ser Pro Gly Lys
 465 470

<210> 2
 <211> 360
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 C2B8 domain deleted heavy chain amino acid sequence

<400> 2
 Met Gly Trp Ser Leu Ile Leu Leu Phe Leu Val Ala Val Ala Thr Arg
 1 5 10 15

Val Leu Ser Gln Val Gln Leu Gln Gln Pro Gly Ala Glu Leu Val Lys
 20 25 30

Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45

Thr Ser Tyr Asn Met His Trp Val Lys Gln Thr Pro Gly Arg Gly Leu
 50 55 60

Glu Trp Ile Gly Ala Ile Tyr Pro Gly Asn Gly Asp Thr Ser Tyr Asn
 65 70 75 80

Gln Lys Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser
 85 90 95

Thr Ala Tyr Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val
 100 105 110

Tyr Tyr Cys Ala Arg Ser Thr Tyr Tyr Gly Gly Asp Trp Tyr Phe Asn
 115 120 125

Val Trp Gly Ala Gly Thr Thr Val Thr Val Ser Ala Ala Ser Thr Lys
 130 135 140

Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly
 145 150 155 160

Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro
 165 170 175

Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr
 180 185 190

Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val
 195 200 205
 Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn
 210 215 220
 Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro
 225 230 235 240
 Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Gly Gln Pro
 245 250 255
 Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr
 260 265 270
 Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
 275 280 285
 Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
 290 295 300
 Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
 305 310 315 320
 Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
 325 330 335
 Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
 340 345 350
 Ser Leu Ser Leu Ser Pro Gly Lys
 355 360

<210> 3

<211> 1412

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
C2B8 heavy chain nucleotide sequence

<400> 3

atgggttgga gcctcatctt gctcttcctt gtcgctgttg ctacgcgtgt cctgtcccag 60
 gtacaactgc agcagcctgg ggctgagctg gtgaagcctg gggcctcagt gaagatgtcc 120
 tgcaaggctt ctggctacac atttaccagt tacaatatgc actgggtaaa acagacacct 180
 ggtcggggcc tggaatggat tggagctatt tatcccgga atggtgatac ttcctacaat 240
 cagaagttca aaggcaaggc cacattgact gcagacaaat cctccagcac agcctacatg 300
 cagctcagca gcctgacatc tgaggactct gcggtctatt actgtgcaag atcgacttac 360
 tacggcgggtg actggtactt caatgtctgg ggcgcaggga ccacggtcac cgtctctgca 420
 gctagcacca agggcccatc ggtcttcccc ctggcaccct cctccaagag cacctctggg 480
 ggcacagcgg ccctgggctg cctggtcaag gactacttcc ccgaaccggt gacggtgtcg 540
 tggaactcag ggcacctgac cagcggcgtg cacaccttcc cggctgtcct acagtctca 600
 ggactctact ccctcagcag cgtggtgacc gtgccctcca gcagcttggg caccagacc 660
 tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agcagagccc 720
 aaatcttgtg acaaaactca cacatgccca ccgtgcccag cacctgaact cctgggggga 780

```

ccgtcagtct tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct 840
gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 900
tacgtggacg gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 960
agcacgtacc gtgtgggtcag cgtcctcacc gtccctgcacc aggactggct gaatggcaag 1020
gagtacaagt gcaagggtctc caacaaagcc ctcccagccc ccatcgagaa aaccatctcc 1080
aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccggatgagc 1140
tgaccaagaa ccaggtcagc ctgacctgcc tgggtcaaagg cttctatccc agcgacatcg 1200
ccgtggagtg ggagagcaat gggcagcccg agaacaacta caagaccacg cctcccgtgc 1260
tggactccga cggctccttc ttctctaca gcaagctcac cgtggacaag agcaggtggc 1320
agcaggggaa cgtcttctca tgctccgtga tgcatgaggg tctgcacaac cactacacgc 1380
agaagagcct ctccctgtct ccgggtaaat ga 1412

```

<210> 4

<211> 1083

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
C2B8 domain deleted heavy chain nucleotide sequence

<400> 4

```

atggggttga gcctcatctt gctcttcctt gtgctgttg ctacgcgtgt cctgtcccag 60
gtacaactgc agcagcctgg ggctgagctg gtgaagcctg gggcctcagt gaagatgtcc 120
tgcaaggctt ctggctacac atttaccagt tacaatatgc actgggtaaa acagacacct 180
ggtcggggcc tggatggat tggagctatt tatcccgaa atggtgatac ttctacaat 240
cagaagttca aaggcaaggc cacattgact gcagacaaat cctccagcac agcctacatg 300
cagctcagca gcctgacatc tgaggactct gcggtctatt actgtgcaag atcgacttac 360
tacggcggtg actggtactt caatgtctgg ggcgcaggga ccacggtcac cgtctctgca 420
gctagcacca agggcccatc ggtcttcccc ctggcacccct cctccaagag cacctctggg 480
ggcacagcgg ccctgggctg cctgggtcaag gactacttcc ccgaaccggt gacgggtgtc 540
tggaactcag gcgcctgac cagcggcgtg cacaccttcc cggctgtcct acagtcctca 600
ggactctact cctcagcag cgtggtgacc gtgcccctca gcagcttggg caccagacc 660
tacatctgca acgtgaatca caagcccagc aacaccaagg tggacaagaa agttgagccc 720
aaatcttgtg acaaaactca cacatgccc cctgcccag ggcagccccg agaaccacag 780
gtgtacaccc tgcccccatc ccgggatgag ctgaccaaga accaggtcag cctgacctgc 840
ctgggtcaaag gcttctatcc cagcgacatc gccgtggagt gggagagcaa tgggcagccg 900
gagaacaact acaagaccac gcctcccgtg ctggactccg acggctcctt ctctctctac 960
agcaagctca ccgtggacaa gagcagggtg cagcagggga acgtcttctc atgctccgtg 1020
atgcatgagg ctctgcacaa ccactacagc cagaagagcc tctccctgtc tccgggtaaa 1080
tga 1083

```

<210> 5

<211> 708

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
C2B8 light chain nucleotide sequence

<400> 5

```

atggattttc aggtgcagat tatcagcttc ctgctaata gtgcttcagt cataatgtcc 60
agaggacaaa ttgttctctc ccagtctcca gcaatcctgt ctgcatctcc aggggagaag 120
gtcacaatga cttgcagggc cagctcaagt gtaagttaca tccactgggt ccagcagaag 180
ccaggatcct ccccaaacc ctggatttat gccacatcca acctggcttc tggagtccct 240

```

```

gttcgcttca gtggcagtgg gtctgggact tcttactctc tcacaatcag cagagtggag 300
gctgaagatg ctgccactta ttactgccag cagtggacta gtaaccacc caggttcgga 360
ggggggacca agctggaaat caaacgtacg gtggctgcac catctgtctt catcttccc 420
ccatctgatg agcagttgaa atctggaact gcctctgttg tgtgcctgct gaataacttc 480
tatcccagag aggccaaagt acagtggaag gtggataacg ccctccaatc gggtaactcc 540
caggagagtg tcacagagca ggacagcaag gacagcacct acagcctcag cagcaccctg 600
acgctgagca aagcagacta cgagaaacac aaagtctacg cctgcgaagt caccatcag 660
ggcctgagct cgcccgtcac aaagagcttc aacaggggag agtgttga 708

```

<210> 6

<211> 235

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
C2B8 light chain amino acid sequence

<400> 6

```

Met Asp Phe Gln Val Gln Ile Ile Ser Phe Leu Leu Ile Ser Ala Ser
 1             5             10             15

Val Ile Met Ser Arg Gly Gln Ile Val Leu Ser Gln Ser Pro Ala Ile
          20             25             30

Leu Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Arg Ala Ser
          35             40             45

Ser Ser Val Ser Tyr Ile His Trp Phe Gln Gln Lys Pro Gly Ser Ser
          50             55             60

Pro Lys Pro Trp Ile Tyr Ala Thr Ser Asn Leu Ala Ser Gly Val Pro
          65             70             75             80

Val Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile
          85             90             95

Ser Arg Val Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Trp
          100            105            110

Thr Ser Asn Pro Pro Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
          115            120            125

Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
          130            135            140

Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe
          145            150            155            160

Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln
          165            170            175

Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser
          180            185            190

Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu
          195            200            205

```

Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser
 210 215 220

Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 225 230 235

<210> 7
 <211> 354
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 HuCC49 domain deleted heavy chain amino acid sequence

<400> 7
 Met Gly Trp Ser Leu Ile Leu Leu Phe Leu Val Ala Val Ala Thr Arg
 1 5 10 15
 Val Leu Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Val Lys
 20 25 30
 Pro Gly Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Thr Phe
 35 40 45
 Thr Asp His Ala Ile His Trp Val Lys Gln Asn Pro Gly Gln Arg Leu
 50 55 60
 Glu Trp Ile Gly Tyr Phe Ser Pro Gly Asn Asp Asp Phe Lys Tyr Asn
 65 70 75 80
 Glu Arg Phe Lys Gly Lys Ala Thr Leu Thr Ala Asp Thr Ser Ala Ser
 85 90 95
 Thr Ala Tyr Val Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val
 100 105 110
 Tyr Phe Cys Thr Arg Ser Leu Asn Met Ala Tyr Trp Gly Gln Gly Thr
 115 120 125
 Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro
 130 135 140
 Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly
 145 150 155 160
 Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn
 165 170 175
 Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln
 180 185 190
 Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser
 195 200 205

Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser
 210 215 220
 Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr
 225 230 235 240
 His Thr Cys Pro Pro Cys Pro Gly Gln Pro Arg Glu Pro Gln Val Tyr
 245 250 255
 Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu
 260 265 270
 Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp
 275 280 285
 Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val
 290 295 300
 Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp
 305 310 315 320
 Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His
 325 330 335
 Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro
 340 345 350

Gly Lys

<210> 8

<211> 1065

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

HuCC49 domain deleted heavy chain nucleotide sequence

<400> 8

atgggttgga gctcatctt gctcttcctt gtcgctgttg ctacgcgtgt cctgtcccag 60
 gtccagctgg tgcagtccgg cgctgaggtg gtgaaacctg gggcttccgt gaagatttcc 120
 tgcaaggcaa gcggctacac cttcactgat cacgcaatcc actgggtgaa acagaatcct 180
 ggacagcgcc tggagtggat tggatatctt tctcccggaa acgatgattt taagtacaat 240
 gagaggttca agggcaaggc cacactgact gcagacacat ctgccagcac tgcctacgtg 300
 gagctctcca gcctgagatc cgaggatact gcagtgtact tctgcacaag atccctgaat 360
 atggcctact ggggacaggg aaccctggtc accgtctcca gcgctagcac caagggccca 420
 tcggtcttcc ccttggcacc ctctccaag agcacctctg ggggcacagc ggccctgggc 480
 tgcttggtca aggactactt cccgaaaccg gtgacggtgt cgtggaactc aggcgccttg 540
 accagcgcg tgacacactt cccggctgtc ctacagtcct caggactcta ctccctcagc 600
 agcgtggtga ccgtgccttc cagcagcttg ggcacccaga cctacatctg caacgtgaat 660
 cacaagccca gcaacaccaa ggtggacaag aaagttgagc ccaaattctt tgacaaaact 720
 cacacatgcc caccgtgccc agggcagccc cgagaaccac aggtgtacac cctgccccca 780
 tcccgggatg agctgaccaa gaaccaggtc agcctgacct gcctgggtcaa aggtctctat 840
 cccagcgaca tcgccgtgga gtgggagagc aatgggcagc cggagaacaa ctacaagacc 900
 acgcctcccg tgctggactc cgacggctcc ttcttctctt acagcaagct caccgtggac 960
 aagagcaggt ggcagcaggg gaacgtcttc tcatgctccg tgatgcatga ggctctgcac 1020
 aaccactaca cgcagaagag cctctccctg tctccgggta aatga 1065

<210> 9
 <211> 240
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 HuCC49 light chain amino acid sequence

<400> 9
 Met Asp Ser Gln Ala Gln Val Leu Met Leu Leu Leu Leu Trp Val Ser
 1 5 10 15
 Gly Thr Cys Gly Asp Ile Val Met Ser Gln Ser Pro Asp Ser Leu Ala
 20 25 30
 Val Ser Leu Gly Glu Arg Val Thr Leu Asn Cys Lys Ser Ser Gln Ser
 35 40 45
 Leu Leu Tyr Ser Gly Asn Gln Lys Asn Tyr Leu Ala Trp Tyr Gln Gln
 50 55 60
 Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ala Ser Ala Arg
 65 70 75 80
 Glu Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp
 85 90 95
 Phe Thr Leu Thr Ile Ser Ser Val Gln Ala Glu Asp Val Ala Val Tyr
 100 105 110
 Tyr Cys Gln Gln Tyr Tyr Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr
 115 120 125
 Lys Leu Glu Leu Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe
 130 135 140
 Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys
 145 150 155 160
 Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val
 165 170 175
 Asp Asn Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln
 180 185 190
 Asp Ser Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser
 195 200 205
 Lys Ala Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His
 210 215 220
 Gln Gly Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 225 230 235 240

<210> 10
 <211> 723
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 HuCC49 light chain nucleotide sequence

<400> 10
 atggatagcc aggccaggt gtcctgctc ctgctgctgt gggtgagcgg cacatgcggc 60
 gacatcgtga tgagccagtc tccagactcc ctggccgtgt ccctgggcga gagggtgact 120
 ctgaattgca agtccagcca gtccctgctc tatagcggaa atcagaagaa ctatctcgcc 180
 tggtatcagc agaaaccagg gcagagccct aaactgctga tttactgggc atccgctagg 240
 gaatccggcg tgcctgatcg cttcagcggc agcggatctg ggacagactt cactctgaca 300
 atcagcagcg tgcaggcaga agacgtggca gtctattatt gtcagcagta ttatagctat 360
 cccctcacat tggcgctgg caccaagctg gaactgaaac gtacgggtggc tgcaccatct 420
 gtcttcatct tcccgccatc tgatgagcag ttgaaatctg gaactgcctc tgttgtgtgc 480
 ctgctgaata acttctatcc cagagaggcc aaagtacagt ggaagggtgga taacgccctc 540
 caatcgggta actcccagga gagtgtcaca gagcaggaca gcaaggacag cacctacagc 600
 ctcagcagca ccctgacgct gagcaaagca gactacgaga aacacaaagt ctacgcctgc 660
 gaagtcaccc atcagggcct gagctcgccc gtcacaaaga gcttcaacag gggagagtgt 720
 tga 723

<210> 11
 <211> 468
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 C5E10 heavy chain amino acid sequence

<400> 11
 Met Ala Val Leu Ala Leu Leu Phe Cys Leu Val Thr Phe Pro Ser Cys
 1 5 10 15
 Ile Leu Ser Gln Val Gln Leu Lys Glu Ser Gly Pro Gly Leu Val Ala
 20 25 30
 Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu
 35 40 45
 Thr Asp Tyr Gly Val Asn Trp Val Arg Gln Pro Pro Gly Lys Gly Leu
 50 55 60
 Glu Trp Leu Gly Met Ile Trp Asp Asn Gly Arg Thr Asp Tyr Asn Ser
 65 70 75 80
 Ala Leu Lys Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln
 85 90 95
 Val Phe Leu Lys Met Thr Ser Leu Gln Thr Asp Asp Thr Ala Arg Tyr
 100 105 110
 Tyr Cys Ala Arg Cys Tyr Tyr Gly Ser Ser Pro Tyr Phe Asp Tyr Trp
 115 120 125

Gly	Gln	Gly	Thr	Thr	Leu	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	130	135	140
Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	145	150	155
Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	165	170	175
Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	180	185	190
Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	195	200	205
Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	210	215	220
His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	225	230	235
Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	245	250	255
Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	Leu	260	265	270
Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	Ser	275	280	285
His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	Glu	290	295	300
Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	Thr	305	310	315
Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	Asn	325	330	335
Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	Pro	340	345	350
Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	Gln	355	360	365
Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Asp	Glu	Leu	Thr	Lys	Asn	Gln	Val	370	375	380
Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	Val	385	390	395
Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	Pro	405	410	415
Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	Thr	420	425	430

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
 435 440 445

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 450 455 460

Ser Pro Gly Lys
 465

<210> 12

<211> 358

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

C5E10 domain deleted heavy chain amino acid sequence

<400> 12

Met Ala Val Leu Ala Leu Leu Phe Cys Leu Val Thr Phe Pro Ser Cys
 1 5 10 15

Ile Leu Ser Gln Val Gln Leu Lys Glu Ser Gly Pro Gly Leu Val Ala
 20 25 30

Pro Ser Gln Ser Leu Ser Ile Thr Cys Thr Val Ser Gly Phe Ser Leu
 35 40 45

Thr Asp Tyr Gly Val Asn Trp Val Arg Gln Pro Pro Gly Lys Gly Leu
 50 55 60

Glu Trp Leu Gly Met Ile Trp Asp Asn Gly Arg Thr Asp Tyr Asn Ser
 65 70 75 80

Ala Leu Lys Ser Arg Leu Ser Ile Asn Lys Asp Asn Ser Lys Ser Gln
 85 90 95

Val Phe Leu Lys Met Thr Ser Leu Gln Thr Asp Asp Thr Ala Arg Tyr
 100 105 110

Tyr Cys Ala Arg Cys Tyr Tyr Gly Ser Ser Pro Tyr Phe Asp Tyr Trp
 115 120 125

Gly Gln Gly Thr Thr Leu Thr Val Ser Ser Ala Ser Thr Lys Gly Pro
 130 135 140

Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr
 145 150 155 160

Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr
 165 170 175

Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro
 180 185 190

Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr
 195 200 205

Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys Asn Val Asn
 210 215 220
 His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser
 225 230 235 240
 Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Gly Gln Pro Arg Glu
 245 250 255
 Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn
 260 265 270
 Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
 275 280 285
 Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
 290 295 300
 Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
 305 310 315 320
 Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
 325 330 335
 Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
 340 345 350
 Ser Leu Ser Pro Gly Lys
 355

<210> 13

<211> 1407

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
C5E10 heavy chain nucleotide sequence

<400> 13

```

atggctgtct tagcgtact cttctgctg gtaacattcc caagctgtat cttttccag 60
gtgcagctga aggagtcagg acctggcctg gtggcgccct cacagagcct gtccatcaca 120
tgcaccgtct cagggttctc attaacccgac tatggtgtaa actgggttcg ccagcctcca 180
ggaaagggtc tggagtggct tggaaatgata tgggataatg gaagaacaga ctataattca 240
gctctcaaat ccagactgag catcaacaag gacaactcca agagccaagt tttcttaaaa 300
atgaccagtc tgcaaaactga tgacacagcc aggtactact gtgccagatg ctattacggt 360
agtagccctt actttgacta ctggggccaa ggcaccactc tcaccgtctc ctacagtagc 420
accaagggcc catcggctctt ccccttgcca cctcctcca agagcacctc tgggggcaca 480
gcggccctgg gctgcctggt caaggactac ttccccgaac cggtgacggt gtcgtggaac 540
tcaggcgccc tgaccagcgg cgtgcacacc tcccggctg tcctacagtc ctacaggactc 600
tactccctca gcagcgtggt gaccgtgccc tccagcagct tgggcaccca gacctacatc 660
tgcaacgtga atcacaagcc cagcaacacc aaggtggaca agaaagttga gcccaaattc 720
tgtgacaaaa ctcacacatg cccaccgtgc ccagcacctg aactcctggg gggaccgtca 780
gtcttctctt tcccccaaaa acccaaggac accctcatga tctcccgac ccctgaggtc 840
acatgcgtgg tgggtggacgt gagccacgaa gaccctgagg tcaagttcaa ctggtacgtg 900
gacggcgtgg aggtgcataa tgccaagaca aagccgcggg aggagcagta caacagcacg 960

```

taccgtgtgg	tcagcgtcct	caccgtcctg	caccaggact	ggctgaatgg	caaggagtac	1020
aagtgaagg	tctccaacaa	agccctccca	gcccccatcg	agaaaacccat	ctccaaagcc	1080
aaagggcagc	cccgagaacc	acaggtgtac	acccctgcccc	catcccggga	tgagctgacc	1140
aagaaccagg	tcagcctgac	ctgcctggtc	aaaggcttct	atcccagcga	catcgccgtg	1200
gagtgggaga	gcaatgggca	gccggagaa	aactacaaga	ccacgcctcc	cgtgctggac	1260
tccgacggct	ccttcttctc	ctacagcaag	ctcaccgtgg	acaagagcag	gtggcagcag	1320
gggaacgtct	tctcatgctc	cgtgatgcat	gaggctctgc	acaaccacta	cacgcagaag	1380
agcctctccc	tgtctccggg	taaatga				1407

<210> 14

<211> 1077

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

C5E10 domain deleted heavy chain nucleotide sequence

<400> 14

atggctgtct	tagcgtact	cttctgcctg	gtaacattcc	caagctgtat	cctttccag	60
gtgcagctga	aggagtcagg	acctggcctg	gtggcgccct	cacagagcct	gtccatcaca	120
tgaccgtct	cagggttctc	attaaccgac	tatgggtgtaa	actgggttcg	ccagcctcca	180
ggaaagggct	tggagtggct	tggaaatgata	tgggataatg	gaagaacaga	ctataattca	240
gctctcaaat	ccagactgag	catcaacaag	gacaactcca	agagccaagt	tttcttaaaa	300
atgaccagtc	tgcaaaactga	tgacacagcc	aggtactact	gtgccagatg	ctattacggt	360
agtagccctt	actttgacta	ctggggccaa	ggcaccactc	tcaccgtctc	ctcagctagc	420
accaagggcc	catcggtctt	ccccctggca	ccctcctcca	agagcacctc	tgggggcaca	480
gcggccctgg	gctgcctggg	caaggactac	ttccccgaac	cggtgacggg	gtcgtggaac	540
tcaggcgccc	tgaccagcgg	cgtgcacacc	ttcccggtcg	tcctacagtc	ctcaggactc	600
tactccctca	gcagcgtggg	gaccgtgccc	tccagcagct	tgggcaccca	gacctacatc	660
tgcaacgtga	atcacaagcc	cagcaacacc	aaggtggaca	agaaagttag	gccccaaatct	720
tgtgacaaaa	ctcacacatg	cccaccgtgc	ccagggcagc	cccgagaacc	acaggtgtac	780
accctgcccc	catcccgga	tgagctgacc	aagaaccagg	tcagcctgac	ctgcctgggtc	840
aaaggcttct	atcccagcga	catcgccgtg	gagtgggaga	gcaatgggca	gccggagaa	900
aactacaaga	ccacgcctcc	cgtgctggac	tccgacggct	ccttcttctc	ctacagcaag	960
ctcaccgtgg	acaagagcag	gtggcagcag	gggaacgtct	tctcatgctc	cgtgatgcat	1020
gaggctctgc	acaaccacta	cacgcagaag	agcctctccc	tgtctccggg	taaatga	1077

<210> 15

<211> 717

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic

C5E10 light chain nucleotide sequence

<400> 15

atgggcatca	agatggagtc	acattctctg	gtctttgtat	acatgttgct	gtggttgtct	60
ggtgttgaag	gagacattgt	gatgatccag	tctcacaat	tcatgtccac	atcagtagga	120
gacagggtca	gcattccctg	caaggccagt	caggatgtgg	gtactgctgt	cgcctggtat	180
caacagaaac	caggacaatc	tcctaaacta	ctgatttact	ggatcatccac	ccggcacact	240
ggagtccctg	atcgcttcac	aggcagtggg	tctgggacag	atttctactc	caccattagc	300
aatgtgcagt	ctgaagactt	ggcagattat	ttctgtcagt	tatatagcag	ctatcctctc	360
acgttcggag	gggggaccaa	gctggaaatc	aaacgtacgg	tggctgcacc	atctgtcttc	420
atcttccccg	catctgatga	gcagttgaaa	tctggaactg	cctctgttgt	gtgcctgctg	480

```

aataacttct atcccagaga ggccaaagta cagtgggaagg tggataacgc cctccaatcg 540
ggtaactccc aggagagtgt cacagagcag gacagcaagg acagcaccta cagcctcagc 600
agcaccctga cgctgagcaa agcagactac gagaaacaca aagtctacgc ctgcgaagtc 660
acccatcagg gcctgagctc gcccgtcaca aagagcttca acaggggaga gtgttga 717

```

<210> 16

<211> 238

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
C5E10 light chain amino acid sequence

<400> 16

```

Met Gly Ile Lys Met Glu Ser His Ser Leu Val Phe Val Tyr Met Leu
  1              5              10              15

Leu Trp Leu Ser Gly Val Glu Gly Asp Ile Val Met Ile Gln Ser His
      20              25              30

Lys Phe Met Ser Thr Ser Val Gly Asp Arg Val Ser Ile Thr Cys Lys
      35              40              45

Ala Ser Gln Asp Val Gly Thr Ala Val Ala Trp Tyr Gln Gln Lys Pro
      50              55              60

Gly Gln Ser Pro Lys Leu Leu Ile Tyr Trp Ser Ser Thr Arg His Thr
      65              70              75              80

Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr
      85              90              95

Leu Thr Ile Ser Asn Val Gln Ser Glu Asp Leu Ala Asp Tyr Phe Cys
      100              105              110

Gln Leu Tyr Ser Ser Tyr Pro Leu Thr Phe Gly Gly Gly Thr Lys Leu
      115              120              125

Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro
      130              135              140

Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu
      145              150              155              160

Asn Asn Phe Tyr Pro Arg Glu Ala Lys Val Gln Trp Lys Val Asp Asn
      165              170              175

Ala Leu Gln Ser Gly Asn Ser Gln Glu Ser Val Thr Glu Gln Asp Ser
      180              185              190

Lys Asp Ser Thr Tyr Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala
      195              200              205

Asp Tyr Glu Lys His Lys Val Tyr Ala Cys Glu Val Thr His Gln Gly
      210              215              220

```

Leu Ser Ser Pro Val Thr Lys Ser Phe Asn Arg Gly Glu Cys
 225 230 235

<210> 17

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
 short amino acid spacer

<400> 17

Gly Gly Ser Ser Gly Gly Gly Gly Ser Gly
 1 5 10